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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=11; hr=13; min=38; sec=8; ms=962;]

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Application No: 10518414 Version No: 2.0

Input Set:

Output Set:

Started: 2008-02-26 18:40:10.548
Finished: 2008-02-26 18:40:12.027
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 479 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

SEQUENCE LISTING

<110> Chr. Hansen A/S

Maarten van den Brink, Johannes
Harboe, Marianne K
Petersen, Steen Guldager
Rahbek-Nielsen, Henrik

<120> IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE POLYPEPTIDE IN
A RECOMBINANT HOST ORGANISM

<130> P1031US00

<140> 10518414

<141> 2005-08-30

<150> PA 2002 0092

<151> 2002-06-17

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 323

<212> PRT

<213> Bos taurus

<400> 1

Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr
1 5 10 15

Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu
20 25 30

Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys
35 40 45

Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser
50 55 60

Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly
65 70 75 80

Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile
85 90 95

Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp
100 105 110

Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro
115 120 125

Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn
130 135 140

Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn
145 150 155 160

Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr
165 170 175

Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln
180 185 190

Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu
195 200 205

Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly
210 215 220

Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
225 230 235 240

Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
245 250 255

Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
260 265 270

Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
275 280 285

Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
290 295 300

Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
305 310 315 320

Lys Ala Ile

<210> 2
<211> 1142
<212> DNA
<213> artificial

<220>
<223> DNA fragment comprising a DNA fragment of 1138 bp designed to comprise a N-H-T glycosylation site and unique SalI and XhoI sites for cloning purposes (modB-XS).

<400> 2

cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcactcgcat ccccctctac	60
aaggcaagt ctctgcgtaa ggctctcaag gaggcaggc tgctcgagga ttccctgcag	120
aagcagcagt acggcatcag ctctaagtac agcggttgc gcgaggtggc cagcgtgcct	180
ctcactaact acctggacag ccagttactt ggttaagatct accttggcac tccccctcag	240
gagttcaccc ttctgttcga tactggttcc agcgacttct gggttccctc catctactgt	300
aagagcaacg cttgcaagaa ccaccagcgc ttcgatcctc gcaagtccag cacttccag	360
aaccttggca agccccttc catccactac ggtactggca gcatgcaggg tatccttggc	420
tacgacaccc ttaccgtgtc caacatcgtc gatattcagc agaccgtggg tctgagcacc	480
caggagcctg gcgatgtctt cacttacgcc gagttcgatg gtatcctcg catggcttac	540
ccctccctgg cctctgagta ctctatccct gtgttcgaca acatgatgaa ccgccacctc	600
gtcgctcagg atctgttca gctgtacatg gaccgtaacg gtcaggagtc catgcttact	660
ctgggcgcca tcgatccctc ttactacacc gggtccctcc actgggttcc tgtgaccgtc	720
cagcagtact ggcagttcac cgtggacagc gtcactatct ccggcgtgg tggcttgc	780
gagggtggct gtcaggccat cttgtataact ggtaccagca agctcgctgg cccctccagc	840
gacatcctga acatccagca ggctatcggt gccaccaga accagtacgg cgagttcgat	900
atcgactgctgataaaccttcc ttacatgcct actgtggttt tcgagatcaa cggtaagatg	960
tacccctta ctcctctgc ttacacttcc caggatcagg gttctgtac ctctgggttc	1020
cagtctgaga accacagcca gaagtggatc cttggcgatg tcttcatccg cgagtactac	1080
tccgtcttcg accgtgccaa caacctggtg ggtctcgcta aggccatctg atcctctaga	1140
gt	1142

<210> 3
<211> 408
<212> DNA
<213> artificial

<220>
<223> an approximately 410 bp SalI-SphII I fragment made using
synthetic oligonucleotides (SEQ ID XXX-1)

<400> 3
cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcactcgcat cccctctac 60

aaggcaagt ctctgcgtaa ggctctcaag gggcacggc tgctcgagga tttccctgcag 120

aagcagcagt acggcatcaag ctctaagtac agcggttgc gcgaggtggc cagcgtgcct 180

ctcactaact acctggacag ccagtacttc ggtaagatct accttggcac tccccctcag 240

gagttcaccc ttctgttcga tactggttcc agcgacttct gggttccctc catctactgt 300

aagagcaacg cttgcaagaa ccaccagcgc ttcgatcctc gcaagtccag cacttccag 360

aacattggca agccccttc catccactac ggtactggca gcatgcag 408

<210> 4
<211> 233
<212> DNA
<213> artificial

<220>
<223> an approximately 220 bp SphI-BsrGI fragment made using synthetic
oligonucleotides (SEQ ID XXX-2)

<400> 4
gcagcatgca gggtatcctt ggctacgaca ccgttaccgt gtccaaacatc gtcgatattc 60

agcagaccgt gggctgagc acccaggagc ctggcgatgt cttcaattac gccgagttcg 120

atggtatcct cggcatggct taccctccc tggcctctga gtactctatc cctgtgttcg 180

acaacatgat gaaccgccac ctcgtcgctc aggatctgtt cagcgtgtac atg 233

<210> 5
<211> 200
<212> DNA
<213> Artificial

<220>
<223> an approximately 190 bp BsrGI-KpnI fragment made using synthetic
oligonucleotides (SEQ ID XXX-3)

<400> 5
gcgtgtacat ggaccgtaac ggtcaggagt ccatgcttac tctggcgcc atcgatccct 60

cttactacac cggttccctc cactgggttc ctgtgaccgt ccagcgtac tggcagttca 120

ccgtggacag cgtcactatac tccggcgtgg ttgtggcttgcgagggtggc tgcgtcaggcca 180

tccttgatac tggtaccaggc 200

<210> 6
<211> 334
<212> DNA
<213> artificial

<220>
<223> an approximately 320 bp KpnI-XbaI fragment made using synthetic oligonucleotides (SEQ ID XXX-4)

<400> 6
ctggtaaccag caagctcgac ggcccccata ggcgacatcct gaacatccag caggctatcg 60
gtgccaccca gaaccagtac ggcgagttcg atatcgactg cgataacctt tcttacatgc 120
ctactgtggt ttccgagatc aacggtaaga tgtaccctt tactccttct gcttacactt 180
cccaggatca gggctctgt acctctgggt tccagtcga gaaccacagg cagaagtgg 240
tccttggcga tgtcttcata cgcgagttact actccgttctt cgaccgtgcc aacaacctgg 300
tgggtctcgc taaggccatc tgatcctcta gagt 334

<210> 7
<211> 334
<212> DNA
<213> artificial

<220>
<223> a modified KpnI-XbaI fragment designed for construction of the modBM gene (SEQ ID XXX-5).

<400> 7
ctggtaaccag caagctcgac ggcccccata ggcgacatcct gaacatccag caggctatcg 60
gtgccaccca gaaccagtac ggcgagttcg atatcgactg cgataacctt tcttacatgc 120
ctactgtggt ttccgagatc aacggtaaga tgtaccctt tactccttct gcttacactt 180
cccaggatca gggctctgt acctctgggt tccagtcga gaaccacacc cagaagtgg 240
tccttggcga tgtcttcata cgcgagttact actccgttctt cgaccgtgcc aacaacctgg 300
tgggtctcgc taaggccatc tgatcctcta gagt 334

<210> 8
<211> 66
<212> DNA
<213> artificial

<220>
<223> synthetic polylinker (SalI-SphI-BsrGI-KpnI-XbaI) (SEQ ID XXX-6)

<400> 8
ggccaggcgc gccttccatg gaagaatgcg gcccgtaaac catcgatggc tcgagttggc 60

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 9
catgtacacg ctgaacagat cctgagc 27

<210> 10
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 10
cgtcgaccgc tacggtgact gacacctggc gtaccgacaa ctccaccgag atcaactcgca 60
tccccctcta caag 74